

Figure 1 : Alignment of the BASB040 polynucleotide sequences.
Identity to SeqID No:1 is indicated by a dot.

	* 20 *	
Seqid1 :	ATGATGATCAAACCGACCGCCCTGCTCCTG	30
Seqid3 :	30
Seqid5 :		-
	40 * 60	
Seqid1 :	CCGGCTTATTTCCTTCCGCACGCATAC	60
Seqid3 :	60
Seqid5 :		-
	* 80 *	
Seqid1 :	GCGCCTGCCGCCGACCTTCCGAAAACAAG	90
Seqid3 :	90
Seqid5 :	24
	100 * 120	
Seqid1 :	GCGGCGGGTTTCGCATTGTTAAAAACAAA	120
Seqid3 :	120
Seqid5 :	54
	* 140 *	
Seqid1 :	AGCCCCGACACCGAATCAGTTAAATTAAAA	150
Seqid3 :	150
Seqid5 :C.....	84
	160 * 180	
Seqid1 :	CCCAAATTCCCCGTCCGCATCGACACGCAG	180
Seqid3 :	180
Seqid5 :T.....	114

	*	200	*	
Seqid1 :	GATAGTGAAATCAAAGATATGGTCGAAGAA			210
Seqid3 :			210
Seqid5 :	..C.....			144

	220	*	240	
Seqid1 :	CACCTGCCGCTCATCACGCAGCAGCAGGAA			240
Seqid3 :			240
Seqid5 :			174

	*	260	*	
Seqid1 :	GAAGTATTGGACAAGGAACAGACGGGCTTC			270
Seqid3 :			270
Seqid5 :			204

	280	*	300	
Seqid1 :	CTCGCCGAAGAACGCACCGGACAACGTTAAA			300
Seqid3 :			300
Seqid5 :G.....			234

	*	320	*	
Seqid1 :	ACCATGCTCCGCAGCAAAGGCTATTCAGC			330
Seqid3 :			330
Seqid5 :	..G.....			264

	340	*	360	
Seqid1 :	AGCAAAGTCAGCCTGACGGAAAAAGACGGA			360
Seqid3 :			360
Seqid5 :			294

Seqid1 : GCTTATACGGTACACATCACACCCGGGCCG : 390
Seqid3 : : 390
Seqid5 : : 324

400 * 420
Seqid1 : CGCACCAAAATGCCAACGTCGGTGTGCC : 420
Seqid3 : : 420
Seqid5 :C.... : 354

* 440 *
Seqid1 : ATCCTCGCGACATCCTTCAGACGGCAAC : 450
Seqid3 : : 450
Seqid5 : : 384

460 * 480
Seqid1 : CTCGCCGAATACTACCGCAACGCGCTGGAA : 480
Seqid3 : : 480
Seqid5 : : 414

* 500 *
Seqid1 : AACTGGCAGCAGCCGGTAGGCAGTGATTTC : 510
Seqid3 : : 510
Seqid5 :C.... : 444

520 * 540
Seqid1 : GATCAGGACAGTTGGAAAACAGCAAAACT : 540
Seqid3 : : 540
Seqid5 : : 474

* 560 *
Seqid1 : TCCGTCTCGCGCGGTAAACGCGAAAAGGC : 570
Seqid3 :C.... : 570

Seqid5 :C....C. : 504

580 * 600
Seqid1 : TACCCGCTTGC~~A~~AGCTCGGCAACACCCGG : 600
Seqid3 : : 600
Seqid5 :T..G.A. : 534

* 620 *
Seqid1 : GCGGCCGTCAACCCCGATA~~CC~~GCCACCGTC : 630
Seqid3 : : 630
Seqid5 :C. : 564

640 * 660
Seqid1 : GATTGAA~~CG~~T~~CG~~TGGACAGCGGCCGC : 660
Seqid3 : : 660
Seqid5 : : 594

* 680 *
Seqid1 : CCCATCGCCTTCGGCGACTTTGAAATCACC : 690
Seqid3 : : 690
Seqid5 : : 624

700 * 720
Seqid1 : GGCACACAGCGTTACCCCGAACAAATCGTC : 720
Seqid3 : : 720
Seqid5 : : 654

* 740 *
Seqid1 : TCCGGCCTGGCGCGCTTCCAACCGGGCACG : 750
Seqid3 : : 750
Seqid5 :T....T....G..C..T..T.. : 684

	760	*	780	
Seqid1 :	CCCTACGACCTCGACCTGCTGCTCGACTTC	:	780	
Seqid3 :	:	780	
Seqid5 :	..G.....	:	714	

	*	800	*	
Seqid1 :	CAACAGGCACTCGAACAAAACGGGCATTAT	:	810	
Seqid3 :	:	810	
Seqid5 :G.....	:	744	

	820	*	840	
Seqid1 :	TCCGGCGCGTCCGTACAAGCCGACTTCGAC	:	840	
Seqid3 :	:	840	
Seqid5 :	:	774	

	*	860	*	
Seqid1 :	CGTCTCCAAGGCGACCGCGTCCCCGTCAAA	:	870	
Seqid3 :	:	870	
Seqid5 :	..C.....	:	804	

	880	*	900	
Seqid1 :	GTCAGCGTAACCGAGGTCAAACGCCACAAG	:	900	
Seqid3 :	:	900	
Seqid5 :A	:	834	

	*	920	*	
Seqid1 :	CTCGAAACCGGCATCCGCCTCGATTGGAA	:	930	
Seqid3 :	:	930	
Seqid5 :	:	864	

	940	*	960	
Seqid1 :	TACGGTTGGCGGGAAAATCGCCTACGAC	:	960	

Seqid3 : : 960
Seqid5 : : 894

		*	980	*
Seqid1	:	TATTACAACCTCTTCAACAAAGGCTATATC	:	990
Seqid3	:,.....	:	990
Seqid5	:	:	924

* 1040 *

Seqid1 : GAAACCACGCTTGCCGCCGGCATCAGCCAG	: 1050
Seqid3 :: 1050	
Seqid5 :: 984	

	1060	*	1080
Seqid1 :	CCGCGCAACTATCGGGGCAACTACTGGACA	:	1080
Seqid3 :	:	1080
Seqid5 :	:	1014

	*	1100	*	
Seqid1	:	AGCAACGTTCTACAAACCGTTGACCACC	:	1110
Seqid3	:	:	1110
Seqid5	:	:	1044

	1120	*	1140
Seqid1 :	CAAAACCTCGAAAAACGCGCCTTCTCCGGC	:	1140
Seqid3 :	:	1140
Seqid5 :	:	1074

* 1160 *

Seqid1 : GGCATCTGGTATGTGCGCGACCGCGCGGGC : 1170
Seqid3 : : 1170
Seqid5 : ...G..... : 1104

1180 * 1200

Seqid1 : ATCGATGCCAGGCTGGGGGCAGAGTTCTC : 1200
Seqid3 : : 1200
Seqid5 :G..A..... : 1134

* 1220 *

Seqid1 : GCAGAAGGCCGGAAAATCCCCGGCTCGGAT : 1230
Seqid3 : : 1230
Seqid5 :C. : 1164

1240 * 1260

Seqid1 : ATCGATTGGGAAACAGGCCACGCCACGATG : 1260
Seqid3 : : 1260
Seqid5 : G..... : 1194

* 1280 *

Seqid1 : CTGACCGCCTCTTGGAAACGCCAGCTGCTC : 1290
Seqid3 : : 1290
Seqid5 : : 1224

1300 * 1320

Seqid1 : AACAACGTGCTGCATCCGAAAACGGCCAT : 1320
Seqid3 : : 1320
Seqid5 : : 1254

* 1340 *

Seqid1 : TACCTCGACGGAAAATCGGTACGACTTG : 1350
Seqid3 : : 1350
Seqid5 : : 1284

1360 * 1380
Seqid1 : GGCACATTCTGTCCCTCCACCGCGCTGATC : 1380
Seqid3 : : 1380
Seqid5 : : 1314

* 1400 *
Seqid1 : CGCACCTCTGCCGTGCAGGTTATTCCTTC : 1410
Seqid3 : : 1410
Seqid5 : : 1344

1420 * 1440
Seqid1 : ACGCCCGAAAACAAAAACTCGGCACGTTC : 1440
Seqid3 : : 1440
Seqid5 : : 1374

* 1460 *
Seqid1 : ATCATACGCGGACAAGCGGGTTACACCGTT : 1470
Seqid3 : : 1470
Seqid5 : : 1404

1480 * 1500
Seqid1 : GCCCGCGACAATGCCGACGTTCCCTCAGGG : 1500
Seqid3 : : 1500
Seqid5 : : 1434

* 1520 *
Seqid1 : CTGATGTTCCGCAGCGGGCGCGTCTTCC : 1530
Seqid3 : : 1530

Seqid5 : : 1464

1540 * 1560
Seqid1 : GTGCGCGGTTACGAACCTCGACAGCATCGGA : 1560
Seqid3 : : 1560
Seqid5 : : 1494

* 1580 *
Seqid1 : CTTGCCGGCCCGAACGGATCGGTCTGCC : 1590
Seqid3 : : 1590
Seqid5 : : 1524

1600 * 1620
Seqid1 : GAACGCGCCCTCCTGGTGGCAGCCTGGAA : 1620
Seqid3 : : 1620
Seqid5 : : 1554

* 1640 *
Seqid1 : TACCAAATGCCGTTACGCGCACCCCTTCC : 1650
Seqid3 : : 1650
Seqid5 : : 1584

1660 * 1680
Seqid1 : GGCGCGGTGTTCCACGATATGGCGATGCC : 1680
Seqid3 : : 1680
Seqid5 : : 1614

* 1700 *
Seqid1 : GCCGCCAATTCAAACGTATGAAGCTGAAA : 1710
Seqid3 : : 1710
Seqid5 : : 1644

1720 * 1740
Seqid1 : CACGGTTCGGGACTGGCGTGCCTGGTTC : 1740
Seqid3 : : 1740
Seqid5 : : 1674

* 1760 *
Seqid1 : AGCCCGCTTGCGCCGTTTCCTTCGACATC : 1770
Seqid3 : : 1770
Seqid5 : : 1704

1780 * 1800
Seqid1 : GCCTACGGGCACAGCGATAAGAAAATCCGC : 1800
Seqid3 : : 1800
Seqid5 : : 1734

* 1820 *
Seqid1 : TGGCACATCAGCTTGGGAACACGCTTCTAA : 1830
Seqid3 : : 1830
Seqid5 : : 1764

Figure 2 : Alignment of the BASB040 polypeptide sequences.
Identity to SeqID No:2 is indicated by a dot.

* 20 *Seqid2 : MMIKPTALLLPALFFFPHAYAPAADLSENK : 30
Seqid4 : : 30

Seqid6 : : 8

40 * 60
Seqid2 : AAGFALFKNKSPDTESVKLKPFPVRIDTQ : 60
Seqid4 : : 60

Seqid6 :L.... : 38

* 80 *Seqid2 : DSEIKDMVEEHLPLITQQQEEVLDKEQTGF : 90
Seqid4 : : 90

Seqid6 : : 68

100 * 120
Seqid2 : LAEEAPDNVKTMLRSKGYFSSKVSLTEKDG : 120
Seqid4 : : 120

Seqid6 : : 98

* 140 *

Seqid2 : AYTVHITPGPRTKIANVGVAILGDI LSDGN : 150
Seqid4 : : 150
Seqid6 : : 128

160 * 180

Seqid2 : LAEYYRNALENWQQPVGSDFDQDSWENSKT : 180
Seqid4 : : 180
Seqid6 : : 158

* 200 *

Seqid2 : SVLGAVTRKGYPLAKLGNTRA AVNPDTATV : 210
Seqid4 : : 210
Seqid6 :A.....Q.....A : 188

220 * 240

Seqid2 : DLNVVVDSGRPIAFGDFEITGTQR YPEQIV : 240
Seqid4 : : 240
Seqid6 : : 218

* 260 *

Seqid2 : SGLARFQPGTPYDLDLLLDFQQALEQNGHY : 270

Seqid4 : : 270

Seqid6 :M..... : 248

280 * 300

Seqid2 : SGASVQADFDRLQGDRVVKVSVTEVKRHK : 300

Seqid4 : : 300

Seqid6 : : 278

* 320 *

Seqid2 : LETGIRLDSEYGLGGKIA~~YDYYNL~~FNKGYI : 330

Seqid4 : : 330

Seqid6 : : 308

340 * 360

Seqid2 : GSVVWDM~~D~~KYETTLAAGISQPRNYRGNYWT : 360

Seqid4 : : 360

Seqid6 : : 338

* 380 *

Seqid2 : SNVSYNRSTTQNLEKRAFSGGIWYVRDRAG : 390

Seqid4 : : 390

Seqid6 : : 368

400 * 420

Seqid2 : IDARLGAEFLAEGRKIPGSDIDLGNSHATM : 420

Seqid4 : : 420

Seqid6 :A..... : 398

* 440 *

Seqid2 : LTASWKRQLLNNVLHPENGHYLDGKIGTTL : 450

Seqid4 : : 450

Seqid6 : : 428

460 * 480

Seqid2 : GTFLSSTALIRTSARAGYFFT PENKKGTF : 480

Seqid4 : : 480

Seqid6 : : 458

* 500 *

Seqid2 : IIRGQAGYTVARDNADVPSGLMFRSGGASS : 510

Seqid4 : : 510

Seqid6 : : 488

520 * 540

Seqid2 : VRGYELDSIGLAGPNGSVLPERALLVGSLE : 540
Seqid4 : : 540
Seqid6 : : 518

* 560 *

Seqid2 : YQLPFTRTLSGAVFHDMGDAANFKRMKLK : 570
Seqid4 : : 570
Seqid6 : : 548

580 * 600

Seqid2 : HGSQLGVRWFSP LAPFSFDIAYGHSDKKIR : 600
Seqid4 : : 600
Seqid6 : : 578

Seqid2 : WHISLGTRF : 609
Seqid4 : : 609
Seqid6 : : 587

SEQUENCE LISTING

<110> SmithKline Beecham Biologicals S.A.

<120> Novel compounds

<130> BM45339

<160> 11

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1830

<212> DNA

<213> *Neisseria meningitidis*

<400> 1

atgatgatca aaccgaccgc	cctgctcctg	ccggctttat	ttttcttcc	gcacgcatac	60	
gcccgcgc	ccgaccttc	cgaaaaacaag	gcggcggtt	tcgcattgtt	caaaaacaaa	120
agccccgaca	ccgaatcagt	taaattaaaa	cccaaattcc	ccgtccgcac	cgacacgcag	180
gatagtaaaa	tcaaagatat	ggtcgaagaa	cacctgcccgc	tcatcacgca	gcagcaggaa	240
gaagtattgg	acaaggaaca	gacgggcttc	ctcgccgaag	aagcaccgga	caacgttaaa	300
accatgctcc	gcagcaaagg	ctatttcagc	agcaaagtca	gcctgacgga	aaaagacgga	360
gcttatacgg	tacacatcac	accggggcccg	cgcacaaaaa	tgcacaaacgt	cggtgtcgcc	420
atccctcg	acatccttc	agacggcaac	ctcgccgaat	actaccgaa	cgcgctggaa	480
aactggcagc	agccggtagg	cagtgatttc	gatcaggaca	gttggggaaaa	cagcaaaact	540
tccgtcctcg	gcccggtaac	gcgaaaaggc	tacccgcttg	ccaagctcgg	caacacccgg	600
gccccgtca	accccgatac	cgcacccgtc	gatttgaacg	tgcgtcgaa	cagcggccgc	660
cccatcgcc	tcggcgactt	tgaaatcacc	ggcacacagc	gttacccgaa	acaaatcgtc	720
tccggcctgg	cgcgcttcca	accgggcacg	ccctacgacc	tgcacccgt	gctcgacttc	780
caacaggcac	tcgaacaaaa	cgggcattat	tccggcgctg	ccgtacaagc	cgacttcgac	840
cgtctccaag	gcgaccgcgt	ccccgtcaaa	gtcagcgtaa	ccgagggtca	acgccacaag	900
ctcgaaaaccg	gcataccgct	cgattcgaa	tacggtttgg	gcccccaaaat	cgccctacgac	960
tattacaacc	tcttcaacaa	aggctatatac	ggctcggtcg	tctggatata	ggacaaatac	1020
gaaaccacgc	ttggccggcg	catcagccag	ccgcgcacact	atcggggcaa	ctactggaca	1080
agcaacgttt	cctacaacccg	ttcgaccacc	aaaaacctcg	aaaaacgcgc	cttctccggc	1140
ggcatctgg	atgtgcgcga	ccgcgcgggc	atcgatgcca	ggctgggggc	agagtttctc	1200
gcagaaggcc	ggaaaatccc	cggtcggtat	atcgatttgg	gcaacagcca	cgccacgatg	1260
ctgaccgcct	ttggaaaacg	ccagctgctc	aacaacgtgc	tgcacccgaa	aaacggccat	1320

tacctcgacg gcaaaatcg	tacgactttg ggcacattcc	tgtcctccac cgcgcgtgatc	1380
cgcacctctg cccgtgcagg	ttatttcttc acgcccggaaa	acaaaaaaact cggcacgttc	1440
atcatacgcg gacaagcggg	ttacaccgtt gcccggacac	atgccgacgt tccttcaggg	1500
ctgatgttcc gcagcggcgg	cgcgtttcc gtgegggtt	acgaactcga cagcatcgga	1560
cttgcggcc cgaacggatc	ggtcctgccc gaacggccc	tcctggtggg cagcctggaa	1620
taccaactgc cggttacgcg	cacccttcc ggcgcgggtt	tccacgatat gggcgatgcc	1680
gccccaatt tcaaacgtat	gaagctgaaa cacgggtcg	gactgggcgt gcgcgtggttc	1740
agcccgcttg cgccgtttc	cttcgacatc gcctacgggc	acagcgataa gaaaatccgc	1800
tggcacatca gcttggAAC	acgcttctaa		1830

<210> 2

<211> 609

<212> PRT

<213> *Neisseria meningitidis*

<400> 2

Met Met Ile Lys Pro Thr Ala Leu Leu Leu Pro Ala Leu Phe Phe Phe			
1	5	10	15
Pro His Ala Tyr Ala Pro Ala Ala Asp Leu Ser Glu Asn Lys Ala Ala			
20	25	30	
Gly Phe Ala Leu Phe Lys Asn Lys Ser Pro Asp Thr Glu Ser Val Lys			
35	40	45	
Leu Lys Pro Lys Phe Pro Val Arg Ile Asp Thr Gln Asp Ser Glu Ile			
50	55	60	
Lys Asp Met Val Glu Glu His. Leu Pro Leu Ile Thr Gln Gln Gln Glu			
65	70	75	80
Glu Val Leu Asp Lys Glu Gln Thr Gly Phe Leu Ala Glu Glu Ala Pro			
85	90	95	
Asp Asn Val Lys Thr Met Leu Arg Ser Lys Gly Tyr Phe Ser Ser Lys			
100	105	110	
Val Ser Leu Thr Glu Lys Asp Gly Ala Tyr Thr Val His Ile Thr Pro			
115	120	125	
Gly Pro Arg Thr Lys Ile Ala Asn Val Gly Val Ala Ile Leu Gly Asp			
130	135	140	
Ile Leu Ser Asp Gly Asn Leu Ala Glu Tyr Tyr Arg Asn Ala Leu Glu			
145	150	155	160
Asn Trp Gln Gln Pro Val Gly Ser Asp Phe Asp Gln Asp Ser Trp Glu			
165	170	175	
Asn Ser Lys Thr Ser Val Leu Gly Ala Val Thr Arg Lys Gly Tyr Pro			
180	185	190	
Leu Ala Lys Leu Gly Asn Thr Arg Ala Ala Val Asn Pro Asp Thr Ala			

195	200	205
Thr Val Asp Leu Asn Val Val Val Asp Ser Gly Arg Pro Ile Ala Phe		
210	215	220
Gly Asp Phe Glu Ile Thr Gly Thr Gln Arg Tyr Pro Glu Gln Ile Val		
225	230	235
Ser Gly Leu Ala Arg Phe Gln Pro Gly Thr Pro Tyr Asp Leu Asp Leu		
245	250	255
Leu Leu Asp Phe Gln Gln Ala Leu Glu Gln Asn Gly His Tyr Ser Gly		
260	265	270
Ala Ser Val Gln Ala Asp Phe Asp Arg Leu Gln Gly Asp Arg Val Pro		
275	280	285
Val Lys Val Ser Val Thr Glu Val Lys Arg His Lys Leu Glu Thr Gly		
290	295	300
Ile Arg Leu Asp Ser Glu Tyr Gly Leu Gly Gly Lys Ile Ala Tyr Asp		
305	310	315
Tyr Tyr Asn Leu Phe Asn Lys Gly Tyr Ile Gly Ser Val Val Trp Asp		
325	330	335
Met Asp Lys Tyr Glu Thr Thr Leu Ala Ala Gly Ile Ser Gln Pro Arg		
340	345	350
Asn Tyr Arg Gly Asn Tyr Trp Thr Ser Asn Val Ser Tyr Asn Arg Ser		
355	360	365
Thr Thr Gln Asn Leu Glu Lys Arg Ala Phe Ser Gly Gly Ile Trp Tyr		
370	375	380
Val Arg Asp Arg Ala Gly Ile Asp Ala Arg Leu Gly Ala Glu Phe Leu		
385	390	395
Ala Glu Gly Arg Lys Ile Pro Gly Ser Asp Ile Asp Leu Gly Asn Ser		
405	410	415
His Ala Thr Met Leu Thr Ala Ser Trp Lys Arg Gln Leu Leu Asn Asn		
420	425	430
Val Leu His Pro Glu Asn Gly His Tyr Leu Asp Gly Lys Ile Gly Thr		
435	440	445
Thr Leu Gly Thr Phe Leu Ser Ser Thr Ala Leu Ile Arg Thr Ser Ala		
450	455	460
Arg Ala Gly Tyr Phe Phe Thr Pro Glu Asn Lys Lys Leu Gly Thr Phe		
465	470	475
Ile Ile Arg Gly Gln Ala Gly Tyr Thr Val Ala Arg Asp Asn Ala Asp		
485	490	495
Val Pro Ser Gly Leu Met Phe Arg Ser Gly Gly Ala Ser Ser Val Arg		
500	505	510
Gly Tyr Glu Leu Asp Ser Ile Gly Leu Ala Gly Pro Asn Gly Ser Val		
515	520	525

Leu Pro Glu Arg Ala Leu Leu Val Gly Ser Leu Glu Tyr Gln Leu Pro
 530 535 540
 Phe Thr Arg Thr Leu Ser Gly Ala Val Phe His Asp Met Gly Asp Ala
 545 550 555 560
 Ala Ala Asn Phe Lys Arg Met Lys Leu Lys His Gly Ser Gly Leu Gly
 565 570 575
 Val Arg Trp Phe Ser Pro Leu Ala Pro Phe Ser Phe Asp Ile Ala Tyr
 580 585 590
 Gly His Ser Asp Lys Lys Ile Arg Trp His Ile Ser Leu Gly Thr Arg
 595 600 605
 Phe

<210> 3
 <211> 1830
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 3

atgatgatca aaccgaccgc cctgctcctg cccggctttat ttttcttcc	gcacgcatac	60
gcccgcctggccg ccgacaccttc cgaaaaacaag gcggcggtt tcgcattgtt	caaaaaacaaa	120
agccccgaca ccgaatcagt taaattaaaa cccaaattcc ccgtccgcac	cgacacgcag	180
gatagtgaaa tcaaagatat ggtcgaagaa caccctgcccgc tcatacgcac	gcagcaggaa	240
gaagtattgg acaaggaaca gacgggcttc ctcgcccgaag aagcaccgga	caacgttaaa	300
accatgctcc gcagcaaagg ctatttcagc agcaaagtca gcctgacgga	aaaagacgga	360
gcttatacgg tacacatcac accggggcccg cgccacaaaa tcgccaacgt	cggtgtcgcc	420
atcctcggcg acatccttcc agacggcaac ctcgcccgaat actaccgaa	cgcgtggaa	480
aactggcagc agccggtagg cagtgatttc gatcaggaca gttggggaaaa	cagaaaaact	540
tccgtcctcg gcgcggttaac gcgcaaaaggc tacccgcttg ccaagctcg	caacacccgg	600
gccccgtca accccgatac cgccacccgtc gatggtaacg tcgtcggtga	cagcggccgc	660
cccatcgccct tcggcgactt tgaaatcacc ggcacacacgc gttaccccg	acaaatcgtc	720
tccggcctgg cgcgcttcca accggggcacg ccctacgacc tcgacccgt	gctcgacttc	780
caacaggcac tcgaacaaaa cgggcattat tccggcgctg ccgtacaaggc	cgacttcgac	840
cgtctccaag gcgaccgcgt ccccgtaaa gtcagcgtaa ccgagggtcaa	acgcccacaag	900
ctcgaaaaccg gcatccgcct cgattcgaa tacggtttg gccggaaaaat	cgccctacgac	960
tattacaacc tcttcaacaa aggctatatac ggctcggtcg tctggatat	ggacaaatac	1020
gaaaccacgc ttggccgggg catcagccag cccgcgcaact atcggggcaa	ctactggaca	1080
agcaacgttt cctacaaccc ttgcgaccacc caaaaacctcg aaaaacgcgc	cttctccggc	1140
ggcatctggat atgtgcgcga cccgcgcccc atcgatgcca ggctgggggc	agagtttctc	1200
gcagaaggcc gaaaaatccc cggctcgat atcgatttgg gcaacagcca	cgccacgatg	1260
ctgaccgcct ttggaaacg ccagctgctc aacaacgtgc tgcatccga	aaacggccat	1320

tacctcgacg gcaaaatcg	tacgactttg ggcacattcc	tgtcctccac cgcgctgatc	1380
cgcacctctg cccgtgcagg	ttatcttc acgcccggaaa	acaaaaaaact cggcacgttc	1440
atcatacgcg gacaagcg	ttacaccgtt gcccgcaca	atgcccacgt tccttcagg	1500
ctgatgttcc gcagcggcgg	cgcgttcc gtgcgcgg	acgaactcga cagcatcg	1560
cttgcggcc cgaacggatc	ggtcctgccc gaacgcgccc	tcctggtggg cagcctggaa	1620
taccaactgc cgtttacgc	cacccttcc ggcgcgggt	tccacgatat gggcgatgcc	1680
gccgccaatt tcaaacgtat	gaagctggaaa cacggttcgg	gactgggcgt gcgcgtgg	1740
agcccgcttgcgcgttttcc	cttcgacatc gcctacgggc	acagcgataa gaaaatccgc	1800
tggcacatca gcttggaa	acgcttctaa		1830

<210> 4

<211> 609

<212> PRT

<213> *Neisseria meningitidis*

<400> 4

Met Met Ile Lys Pro Thr Ala Leu Leu Leu Pro Ala Leu Phe Phe Phe			
1	5	10	15
Pro His Ala Tyr Ala Pro Ala Ala Asp Leu Ser Glu Asn Lys Ala Ala			
20	25	30	
Gly Phe Ala Leu Phe Lys Asn Lys Ser Pro Asp Thr Glu Ser Val Lys			
35	40	45	
Leu Lys Pro Lys Phe Pro Val Arg Ile Asp Thr Gln Asp Ser Glu Ile			
50	55	60	
Lys Asp Met Val Glu Glu His Leu Pro Leu Ile Thr Gln Gln Gln Glu			
65	70	75	80
Glu Val Leu Asp Lys Glu Gln Thr Gly Phe Leu Ala Glu Glu Ala Pro			
85	90	95	
Asp Asn Val Lys Thr Met Leu Arg Ser Lys Gly Tyr Phe Ser Ser Lys			
100	105	110	
Val Ser Leu Thr Glu Lys Asp Gly Ala Tyr Thr Val His Ile Thr Pro			
115	120	125	
Gly Pro Arg Thr Lys Ile Ala Asn Val Gly Val Ala Ile Leu Gly Asp			
130	135	140	
Ile Leu Ser Asp Gly Asn Leu Ala Glu Tyr Tyr Arg Asn Ala Leu Glu			
145	150	155	160
Asn Trp Gln Gln Pro Val Gly Ser Asp Phe Asp Gln Asp Ser Trp Glu			
165	170	175	
Asn Ser Lys Thr Ser Val Leu Gly Ala Val Thr Arg Lys Gly Tyr Pro			
180	185	190	
Leu Ala Lys Leu Gly Asn Thr Arg Ala Ala Val Asn Pro Asp Thr Ala			

195	200	205
Thr Val Asp Leu Asn Val Val Val Asp Ser Gly Arg Pro Ile Ala Phe		
210	215	220
Gly Asp Phe Glu Ile Thr Gly Thr Gln Arg Tyr Pro Glu Gln Ile Val		
225	230	235
Ser Gly Leu Ala Arg Phe Gln Pro Gly Thr Pro Tyr Asp Leu Asp Leu		
245	250	255
Leu Leu Asp Phe Gln Gln Ala Leu Glu Gln Asn Gly His Tyr Ser Gly		
260	265	270
Ala Ser Val Gln Ala Asp Phe Asp Arg Leu Gln Gly Asp Arg Val Pro		
275	280	285
Val Lys Val Ser Val Thr Glu Val Lys Arg His Lys Leu Glu Thr Gly		
290	295	300
Ile Arg Leu Asp Ser Glu Tyr Gly Leu Gly Gly Lys Ile Ala Tyr Asp		
305	310	315
Tyr Tyr Asn Leu Phe Asn Lys Gly Tyr Ile Gly Ser Val Val Trp Asp		
325	330	335
Met Asp Lys Tyr Glu Thr Thr Leu Ala Ala Gly Ile Ser Gln Pro Arg		
340	345	350
Asn Tyr Arg Gly Asn Tyr Trp Thr Ser Asn Val Ser Tyr Asn Arg Ser		
355	360	365
Thr Thr Gln Asn Leu Glu Lys Arg Ala Phe Ser Gly Gly Ile Trp Tyr		
370	375	380
Val Arg Asp Arg Ala Gly Ile Asp Ala Arg Leu Gly Ala Glu Phe Leu		
385	390	395
Ala Glu Gly Arg Lys Ile Pro Gly Ser Asp Ile Asp Leu Gly Asn Ser		
405	410	415
His Ala Thr Met Leu Thr Ala Ser Trp Lys Arg Gln Leu Leu Asn Asn		
420	425	430
Val Leu His Pro Glu Asn Gly His Tyr Leu Asp Gly Lys Ile Gly Thr		
435	440	445
Thr Leu Gly Thr Phe Leu Ser Ser Thr Ala Leu Ile Arg Thr Ser Ala		
450	455	460
Arg Ala Gly Tyr Phe Phe Thr Pro Glu Asn Lys Lys Leu Gly Thr Phe		
465	470	475
Ile Ile Arg Gly Gln Ala Gly Tyr Thr Val Ala Arg Asp Asn Ala Asp		
485	490	495
Val Pro Ser Gly Leu Met Phe Arg Ser Gly Gly Ala Ser Ser Val Arg		
500	505	510
Gly Tyr Glu Leu Asp Ser Ile Gly Leu Ala Gly Pro Asn Gly Ser Val		
515	520	525

Leu Pro Glu Arg Ala Leu Leu Val Gly Ser Leu Glu Tyr Gln Leu Pro
 530 535 540
 Phe Thr Arg Thr Leu Ser Gly Ala Val Phe His Asp Met Gly Asp Ala
 545 550 555 560
 Ala Ala Asn Phe Lys Arg Met Lys Leu Lys His Gly Ser Gly Leu Gly
 565 570 575
 Val Arg Trp Phe Ser Pro Leu Ala Pro Phe Ser Phe Asp Ile Ala Tyr
 580 585 590
 Gly His Ser Asp Lys Lys Ile Arg Trp His Ile Ser Leu Gly Thr Arg
 595 600 605
 Phe

<210> 5
 <211> 1764
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 5
 gccggccgacc tttccgaaaa caaggcggcg ggtttcgcat tgttcaaaaa caaaagcccc 60
 gacaccgaat cagtcaaatt aaaacccaaa ttccccgtcc tcatacgacac gcaggacagt 120
 gaaatcaaag atatggtcga agaacacctg ccgcgtcatca cgcagcagca ggaagaagta 180
 ttggacaagg aacagacggg cttcctcgcc gaagaagcgc cggacaacgt taaaacgtat 240
 ctccgcagca aaggctattt cagcagcaaa gtcagcctga cggaaaaaga cggagcttat 300
 acggtagaca tcaacaccggg cccgcgcacc aaaatcgcca acgtcggcgt cgccatcctc 360
 ggcgacatcc tttcagacgg caacctcgcc gaatactacc gcaacgcgt ggaaaaactgg 420
 cagcagccgg taggcagcga tttcgatcag gacagttggg aaaacagcaa aacttccgtc 480
 ctcggcgcgg taacgcgcaa agcctacccg cttgccaagc tcggcaatac gcagggcggcc 540
 gtcaaccccg ataccgcac cggcgatttg aacgtcgtcg tggacagcgg cccggccatc 600
 gccttcggcg actttgaaat caccggcaca cagcggttacc ccgaacaaaat cgttccggc 660
 cttgcgcgtt tccagcccg tatgcgtac gacctcgacc tgctgctcga cttccaacag 720
 ggcgtcgaac aaaacgggca ttattccggc gctgtccgtac aagccgactt cgaccgcctc 780
 caaggcggacc gctgtcccgta caaagtcaac gtaaccgagg tcaaaacgcca caaactcgaa 840
 accggcatcc gcctcgattc ggaatacggt ttggggcggca aaatcgccctc cgactattac 900
 aacctttca acaaaggcta tatcggttcg gtcgtctggg atatggacaa atacgaaacc 960
 acgcttgcgcg cggcatcag ccagccgcgc aactatcggt gcaactactg gacaagcaac 1020
 gtttccatca accgttcgac cacccaaaac ctcgaaaaac ggcgttccgtc cggcggcgtc 1080
 tggatgtgc ggcgttcgac gggcatcgt ggcaggctgg gggcggaaatt tccgcagaa 1140
 ggcggaaaa tccccggcgtc ggctgtcgt tggggcaaca gcaacgcac gatgtcgacc 1200
 gcctttgga aacgcagct gctcaacaac gtgcgtcgtc cggaaaaacgg ccattacctc 1260
 gacggcaaaa tggtacgac tttgggcaca ttctgttcc ccaacggcgt gatccgcacc 1320

tctgcccgtg caggttattt cttcacgccc gaaaacaaaa aactcggcac gttcatcata	1380
cgcggacaag cgggttacac cggtgcccgc gacaatgccc acgttcccttc agggctgatg	1440
ttccgcagcg gggcgcggtc ttccgtgcgc ggttacgaac tcgacagcat cggacttgcc	1500
ggcccaacg gatcggtcct gcccgaacgc gcccctctgg tgggcagcct ggaataccaa	1560
ctgcccgtta cgcgcaccct ttccggcgcg gtgttccacg atatggcga tgccgccc	1620
aatttcaaac gtatgaagct gaaacacggt tcgggactgg gcgtgcgcgt gttcagcccg	1680
cttgcgcccgt tttcccttctga catcgctac gggcacagcg ataagaaaat ccgctggcac	1740
atcagcttgg gaacacgctt ctaa	1764

<210> 6

<211> 587

<212> PRT

<213> *Neisseria meningitidis*

<400> 6

Ala Ala Asp Leu Ser Glu Asn Lys Ala Ala Gly Phe Ala Leu Phe Lys			
1	5	10	15
Asn Lys Ser Pro Asp Thr Glu Ser Val Lys Leu Lys Pro Lys Phe Pro			
20	25	30	
Val Leu Ile Asp Thr Gln Asp Ser Glu Ile Lys Asp Met Val Glu Glu			
35	40	45	
His Leu Pro Leu Ile Thr Gln Gln Gln Glu Glu Val Leu Asp Lys Glu			
50	55	60	
Gln Thr Gly Phe Leu Ala Glu Glu Ala Pro Asp Asn Val Lys Thr Met			
65	70	75	80
Leu Arg Ser Lys Gly Tyr Phe Ser Ser Lys Val Ser Leu Thr Glu Lys			
85	90	95	
Asp Gly Ala Tyr Thr Val His Ile Thr Pro Gly Pro Arg Thr Lys Ile			
100	105	110	
Ala Asn Val Gly Val Ala Ile Leu Gly Asp Ile Leu Ser Asp Gly Asn			
115	120	125	
Leu Ala Glu Tyr Tyr Arg Asn Ala Leu Glu Asn Trp Gln Gln Pro Val			
130	135	140	
Gly Ser Asp Phe Asp Gln Asp Ser Trp Glu Asn Ser Lys Thr Ser Val			
145	150	155	160
Leu Gly Ala Val Thr Arg Lys Ala Tyr Pro Leu Ala Lys Leu Gly Asn			
165	170	175	
Thr Gln Ala Ala Val Asn Pro Asp Thr Ala Thr Ala Asp Leu Asn Val			
180	185	190	
Val Val Asp Ser Gly Arg Pro Ile Ala Phe Gly Asp Phe Glu Ile Thr			
195	200	205	

Gly Thr Gln Arg Tyr Pro Glu Gln Ile Val Ser Gly Leu Ala Arg Phe
210 215 220
Gln Pro Gly Met Pro Tyr Asp Leu Asp Leu Leu Asp Phe Gln Gln
225 230 235 240
Ala Leu Glu Gln Asn Gly His Tyr Ser Gly Ala Ser Val Gln Ala Asp
245 250 255
Phe Asp Arg Leu Gln Gly Asp Arg Val Pro Val Lys Val Ser Val Thr
260 265 270
Glu Val Lys Arg His Lys Leu Glu Thr Gly Ile Arg Leu Asp Ser Glu
275 280 285
Tyr Gly Leu Gly Gly Lys Ile Ala Tyr Asp Tyr Tyr Asn Leu Phe Asn
290 295 300
Lys Gly Tyr Ile Gly Ser Val Val Trp Asp Met Asp Lys Tyr Glu Thr
305 310 315 320
Thr Leu Ala Ala Gly Ile Ser Gln Pro Arg Asn Tyr Arg Gly Asn Tyr
325 330 335
Trp Thr Ser Asn Val Ser Tyr Asn Arg Ser Thr Thr Gln Asn Leu Glu
340 345 350
Lys Arg Ala Phe Ser Gly Gly Val Trp Tyr Val Arg Asp Arg Ala Gly
355 360 365
Ile Asp Ala Arg Leu Gly Ala Glu Phe Leu Ala Glu Gly Arg Lys Ile
370 375 380
Pro Gly Ser Ala Val Asp Leu Gly Asn Ser His Ala Thr Met Leu Thr
385 390 395 400
Ala Ser Trp Lys Arg Gln Leu Leu Asn Asn Val Leu His Pro Glu Asn
405 410 415
Gly His Tyr Leu Asp Gly Lys Ile Gly Thr Thr Leu Gly Thr Phe Leu
420 425 430
Ser Ser Thr Ala Leu Ile Arg Thr Ser Ala Arg Ala Gly Tyr Phe Phe
435 440 445
Thr Pro Glu Asn Lys Lys Leu Gly Thr Phe Ile Ile Arg Gly Gln Ala
450 455 460
Gly Tyr Thr Val Ala Arg Asp Asn Ala Asp Val Pro Ser Gly Leu Met
465 470 475 480
Phe Arg Ser Gly Gly Ala Ser Ser Val Arg Gly Tyr Glu Leu Asp Ser
485 490 495
Ile Gly Leu Ala Gly Pro Asn Gly Ser Val Leu Pro Glu Arg Ala Leu
500 505 510
Leu Val Gly Ser Leu Glu Tyr Gln Leu Pro Phe Thr Arg Thr Leu Ser
515 520 525
Gly Ala Val Phe His Asp Met Gly Asp Ala Ala Asn Phe Lys Arg

530 535 540
Met Lys Leu Lys His Gly Ser Gly Leu Gly Val Arg Trp Phe Ser Pro
545 550 555 560
Leu Ala Pro Phe Ser Phe Asp Ile Ala Tyr Gly His Ser Asp Lys Lys
565 570 575
Ile Arg Trp His Ile Ser Leu Gly Thr Arg Phe
580 585

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7

gggcccgaac ctccgaaata

20

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8

cgagccagcc gagggaaacat a

21

<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9

catagcacca tggccgcccga cctttccga

29

<210> 10
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10

ctagtctaga ttagaaggcgt gttcccaagc 30

<210> 11
<211> 1000
<212> DNA
<213> *Neisseria meningitidis*

<400> 11

aaacggataa tccatttcac gacgggtggaa accgcttccg ccaaatacgcc aacgacactgc	60
cgcgttaacgt ccgaaccgtg attccgcaac gcccgcggccaa aaacccaaagc ccaagccaaa	120
atgcccataat agttggcatt ggcaatcgcg ttaatcggtt tggcgaccag gttcatcagc	180
agcgatttca acacttccac aatgcccggaa ggccggcgggg cggacacatc gcccggcgccc	240
gccaaaacaa tgtgcgtcgg gaaaaccata ccggcgatga cggcggtcag ggctgcggaa	300
aacgtaccaa tgaggtaaag gatgataatc ggcctgatata gtcgccttgcgtt gcctttttgg	360
tgcgtgcgca ttgtggccgc cacaaaaata aataccaaaa ccggcgcgac cgctttgagc	420
gcggccacaa acaggctgcc gaacaaggct gcccggcaagc ccagttgcgg ggaaacccgaa	480
ccgattacga tgcccaacgc caaacccggcg gcaatctgcc tgaccaggct gacgcggccg	540
atcgcatgaa ataaggattt gccgaacgccc ataattcttc cttatgttgt gatatgtttaa	600
aaaatgttgtt atttaaaag aaaactcatt ctctgttgcgtt tttttatccc tcggctgtgt	660
tttaaggttg cgttggatgg ccctatgcag tgccggacag gctttgcgtt atcattcgcc	720
gcaacggttt aattttatgg acgaaaataa atttatttaa tcctgcctat tttccggcac	780
tattccggaaa cgcagcctgt tttccatatg cggattggaa aaaaaatacc ttaaaacaag	840
cagatacatt tccggcgccg cgcacactcc gaaataccgg cggcagatag ccgtctgaag	900
tgtcccgcccg cgtccgaaca acacaaaaac agccgttcga aaccctgtcc gaacagtgtt	960
agaatcgaaa tctgccacac cgatgcacga caccctgtacc	1000